

Vandervegt

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/322,875

DATE: 07/11/2000
TIME: 09:56:00

Input Set : A:\09322875.txt
Output Set : N:\CRF3\07112000\I322875.raw

5 <110> APPLICANT: Chuntharapai, Anan
7 Kim, Kyung Jin
11 <120> TITLE OF INVENTION: DR4 ANTIBODIES AND USES THEREOF
15 <130> FILE REFERENCE: 11669.19US02
19 <140> CURRENT APPLICATION NUMBER: 09/322,875
21 <141> CURRENT FILING DATE: 1999-05-28
25 <150> PRIOR APPLICATION NUMBER: 09/237,299
27 <151> PRIOR FILING DATE: 1999-01-25
31 <160> NUMBER OF SEQ ID NOS: 2
35 <170> SOFTWARE: PatentIn Ver. 2.0
39 <210> SEQ ID NO: 1
41 <211> LENGTH: 1407
43 <212> TYPE: DNA
45 <213> ORGANISM: Homo sapiens
49 <220> FEATURE:
51 <221> NAME/KEY: CDS
53 <222> LOCATION: (1)..(1407)
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61 Met Ala Pro Pro Ala Arg Val His Leu Gly Ala Phe Leu Ala Val 15
63 1 5 10 15
67 act ccg aat ccc ggg agc gca gcg agt ggg aca gag gca gcc gcg gcc 96
69 Thr Pro Asn Pro Gly Ser Ala Ala Ser Gly Thr Glu Ala Ala Ala Ala 30
71 20 25 30
75 aca ccc agc aaa gtg tgg ggc tct tcc gcg ggg agg att gaa cca cga 144
77 Thr Pro Ser Lys Val Trp Gly Ser Ser Ala Gly Arg Ile Glu Pro Arg 45
79 35 40 45
83 ggc ggg ggc cga gga gcg ctc cct acc tcc atg gga cag cac gga ccc 192
85 Gly Gly Gly Arg Gly Ala Leu Pro Thr Ser Met Gly Gln His Gly Pro 60
87 50 55 60
91 agt gcc cgg gcc cgg gca ggg cgc gcc cca gga ccc agg ccg gcg cgg 240
93 Ser Ala Arg Ala Arg Ala Gly Arg Ala Pro Gly Pro Arg Pro Ala Arg 75
95 65 70 75 80
99 gaa gcc agc cct cgg ctc cgg gtc cac aag acc ttc aag ttt gtc gtc 288
101 Glu Ala Ser Pro Arg Leu Arg Val His Lys Thr Phe Lys Phe Val Val 95
103 85 90 95
107 gtc ggg gtc ctg ctg cag gtc gta cct agc tca gct gca acc atc aaa 336
109 Val Gly Val Leu Leu Gln Val Val Pro Ser Ser Ala Ala Thr Ile Lys 110
111 100 105 110
115 ctt cat gat caa tca att ggc aca cag caa tgg gaa cat agc cct ttg 384
117 Leu His Asp Gln Ser Ile Gly Thr Gln Gln Trp Glu His Ser Pro Leu 125
119 115 120 125
123 gga gag ttg tgt cca cca gga tct cat aga tca gaa cgt cct gga gcc 432
125 Gly Glu Leu Cys Pro Pro Gly Ser His Arg Ser Glu Arg Pro Gly Ala 140
127 130 135 140
131 tgt aac cgg tgc aca gag ggt gtg ggt tac acc aat gct tcc aac aat 480
133 Cys Asn Arg Cys Thr Glu Gly Val Gly Tyr Thr Asn Ala Ser Asn Asn

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135	145		150		155		160	
139	ttg	ttt	gct	tgc	ctc	cca	tgt	aca
141	Leu	Phe	Ala	Cys	Leu	Pro	Cys	Thr
143					165		170	
147	aga	agt	ccc	tgc	acc	acg	acc	agg
149	Arg	Ser	Pro	Cys	Thr	Thr	Thr	Arg
151					180		185	
155	gga	act	ttc	cgg	aat	gac	aat	tct
157	Gly	Thr	Phe	Arg	Asn	Asp	Asn	Ser
159					195		200	
163	aca	ggg	tgc	ccc	aga	ggg	atg	gtc
165	Thr	Gly	Cys	Pro	Arg	Gly	Met	Val
167					210		215	
171	agt	gac	atc	gag	tgt	gtc	cac	aaa
173	Ser	Asp	Ile	Glu	Cys	Val	His	Lys
175	225				230		235	
179	tgg	gtg	att	ttg	gtt	gtg	act	ttg
181	Trp	Val	Ile	Leu	Val	Val	Thr	Leu
183					245		250	
187	gtg	ctg	att	gtc	tgt	tgc	atc	ggc
189	Val	Leu	Ile	Val	Cys	Cys	Cys	Ile
191					260		265	
195	aag	tgc	atg	gac	agg	gtg	tgt	ttc
197	Lys	Cys	Met	Asp	Arg	Val	Cys	Phe
199					275		280	
203	cct	ggg	gct	gag	gac	aat	gct	cac
205	Pro	Gly	Ala	Glu	Asp	Asn	Ala	His
207					290		295	
211	tcg	ctg	tcc	act	ttc	gtc	tct	gag
213	Ser	Leu	Ser	Thr	Phe	Val	Ser	Glu
215	305				310		315	
219	gca	gat	ttg	aca	ggg	gtc	act	gta
221	Ala	Asp	Leu	Thr	Gly	Val	Thr	Val
223					325		330	
227	ctg	ctg	gga	ccg	gca	gaa	gct	gaa
229	Leu	Leu	Gly	Pro	Ala	Glu	Ala	Glu
231					340		345	
235	gtt	cca	gca	aat	ggg	gct	gac	ccc
237	Val	Pro	Ala	Asn	Gly	Ala	Asp	Pro
239					355		360	
243	gac	aag	ttt	gca	aac	atc	gtg	ccc
245	Asp	Lys	Phe	Ala	Asn	Ile	Val	Pro
247					370		375	
251	agg	cag	ctg	gac	ctc	acg	aaa	aat
253	Arg	Gln	Leu	Asp	Leu	Thr	Lys	Asn
255	385				390		395	
259	aca	gca	ggc	cca	ggg	gat	gcc	ttg
261	Thr	Ala	Gly	Pro	Gly	Asp	Ala	Leu
263					405		410	

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267 aac aaa act gga cgg aac gcc tcg atc cac acc ctg ctg gat gcc ttg 1296
269 Asn Lys Thr Gly Arg Asn Ala Ser Ile His Thr Leu Leu Asp Ala Leu
271 420 425 430
275 gag agg atg gaa gag aga cat gca aaa gag aag att cag gac ctc ttg 1344
277 Glu Arg Met Glu Glu Arg His Ala Lys Glu Lys Ile Gln Asp Leu Leu
279 435 440 445
283 gtg gac tct gga aag ttc atc tac tta gaa gat ggc aca ggc tct gcc 1392
285 Val Asp Ser Gly Lys Phe Ile Tyr Leu Glu Asp Gly Thr Gly Ser Ala
287 450 455 460
291 gtg tcc ttg gag tga 1407
293 Val Ser Leu Glu
295 465
300 <210> SEQ ID NO: 2
302 <211> LENGTH: 468
304 <212> TYPE: PRT
306 <213> ORGANISM: Homo sapiens
310 <400> SEQUENCE: 2
312 Met Ala Pro Pro Pro Ala Arg Val His Leu Gly Ala Phe Leu Ala Val
314 1 5 10 15
318 Thr Pro Asn Pro Gly Ser Ala Ala Ser Gly Thr Glu Ala Ala Ala Ala
320 20 25 30
324 Thr Pro Ser Lys Val Trp Gly Ser Ser Ala Gly Arg Ile Glu Pro Arg
326 35 40 45
330 Gly Gly Gly Arg Gly Ala Leu Pro Thr Ser Met Gly Gln His Gly Pro
332 50 55 60
336 Ser Ala Arg Ala Arg Ala Gly Arg Ala Pro Gly Pro Arg Pro Ala Arg
338 65 70 75 80
342 Glu Ala Ser Pro Arg Leu Arg Val His Lys Thr Phe Lys Phe Val Val
344 85 90 95
348 Val Gly Val Leu Leu Gln Val Val Pro Ser Ser Ala Ala Thr Ile Lys
350 100 105 110
354 Leu His Asp Gln Ser Ile Gly Thr Gln Gln Trp Glu His Ser Pro Leu
356 115 120 125
360 Gly Glu Leu Cys Pro Pro Gly Ser His Arg Ser Glu Arg Pro Gly Ala
362 130 135 140
366 Cys Asn Arg Cys Thr Glu Gly Val Gly Tyr Thr Asn Ala Ser Asn Asn
368 145 150 155 160
372 Leu Phe Ala Cys Leu Pro Cys Thr Ala Cys Lys Ser Asp Glu Glu Glu
374 165 170 175
378 Arg Ser Pro Cys Thr Thr Thr Arg Asn Thr Ala Cys Gln Cys Lys Pro
380 180 185 190
384 Gly Thr Phe Arg Asn Asp Asn Ser Ala Glu Met Cys Arg Lys Cys Ser
386 195 200 205
390 Thr Gly Cys Pro Arg Gly Met Val Lys Val Lys Asp Cys Thr Pro Trp
392 210 215 220
396 Ser Asp Ile Glu Cys Val His Lys Glu Ser Gly Asn Gly His Asn Ile
398 225 230 235 240
402 Trp Val Ile Leu Val Val Thr Leu Val Val Pro Leu Leu Leu Val Ala
404 245 250 255

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408 Val Leu Ile Val Cys Cys Cys Ile Gly Ser Gly Cys Gly Gly Asp Pro
410      260      265      270
414 Lys Cys Met Asp Arg Val Cys Phe Trp Arg Leu Gly Leu Leu Arg Gly
416      275      280      285
420 Pro Gly Ala Glu Asp Asn Ala His Asn Glu Ile Leu Ser Asn Ala Asp
422      290      295      300
426 Ser Leu Ser Thr Phe Val Ser Glu Gln Gln Met Glu Ser Gln Glu Pro
428 305      310      315      320
432 Ala Asp Leu Thr Gly Val Thr Val Gln Ser Pro Gly Glu Ala Gln Cys
434      325      330      335
438 Leu Leu Gly Pro Ala Glu Ala Glu Gly Ser Gln Arg Arg Arg Leu Leu
440      340      345      350
444 Val Pro Ala Asn Gly Ala Asp Pro Thr Glu Thr Leu Met Leu Phe Phe
446      355      360      365
450 Asp Lys Phe Ala Asn Ile Val Pro Phe Asp Ser Trp Asp Gln Leu Met
452      370      375      380
456 Arg Gln Leu Asp Leu Thr Lys Asn Glu Ile Asp Val Val Arg Ala Gly
458 385      390      395      400
462 Thr Ala Gly Pro Gly Asp Ala Leu Tyr Ala Met Leu Met Lys Trp Val
464      405      410      415
468 Asn Lys Thr Gly Arg Asn Ala Ser Ile His Thr Leu Leu Asp Ala Leu
470      420      425      430
474 Glu Arg Met Glu Glu Arg His Ala Lys Glu Lys Ile Gln Asp Leu Leu
476      435      440      445
480 Val Asp Ser Gly Lys Phe Ile Tyr Leu Glu Asp Gly Thr Gly Ser Ala
482      450      455      460
486 Val Ser Leu Glu
488 465

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VERIFICATION SUMMARY
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